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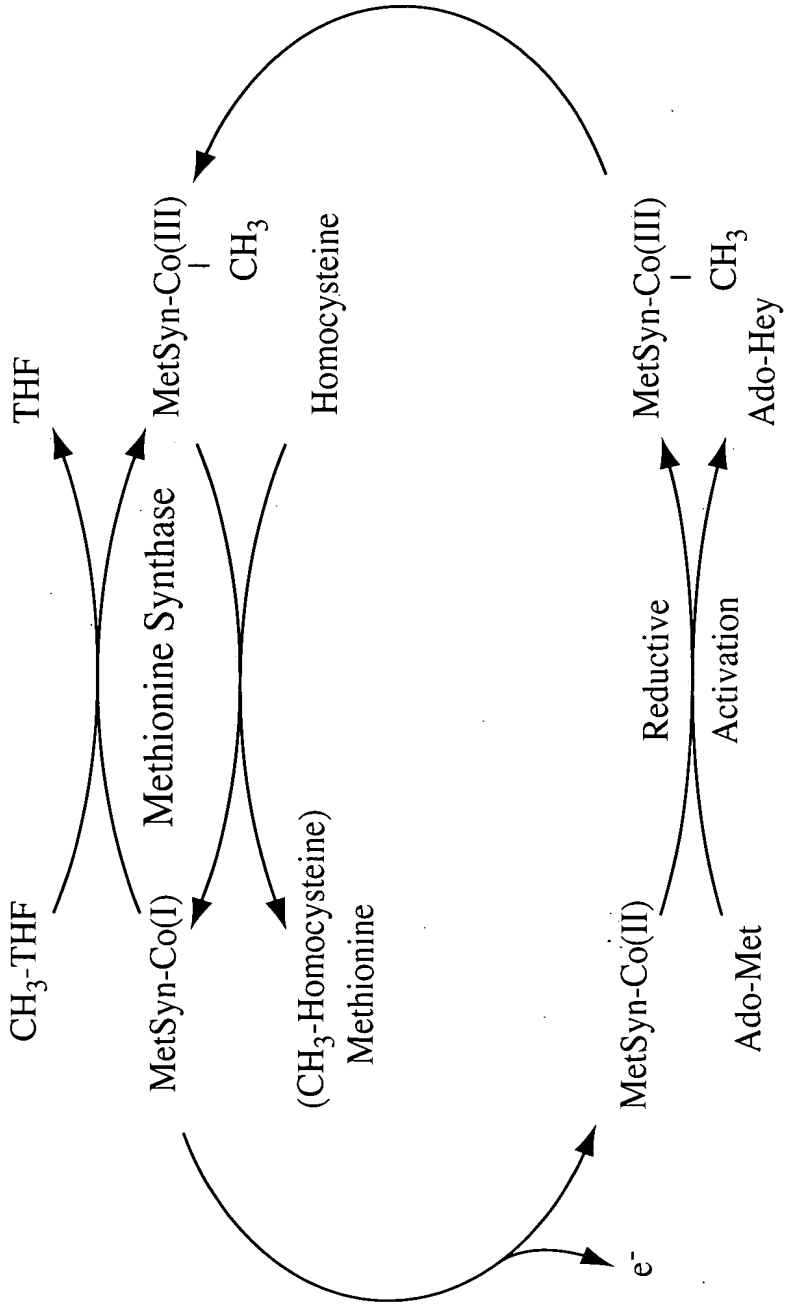
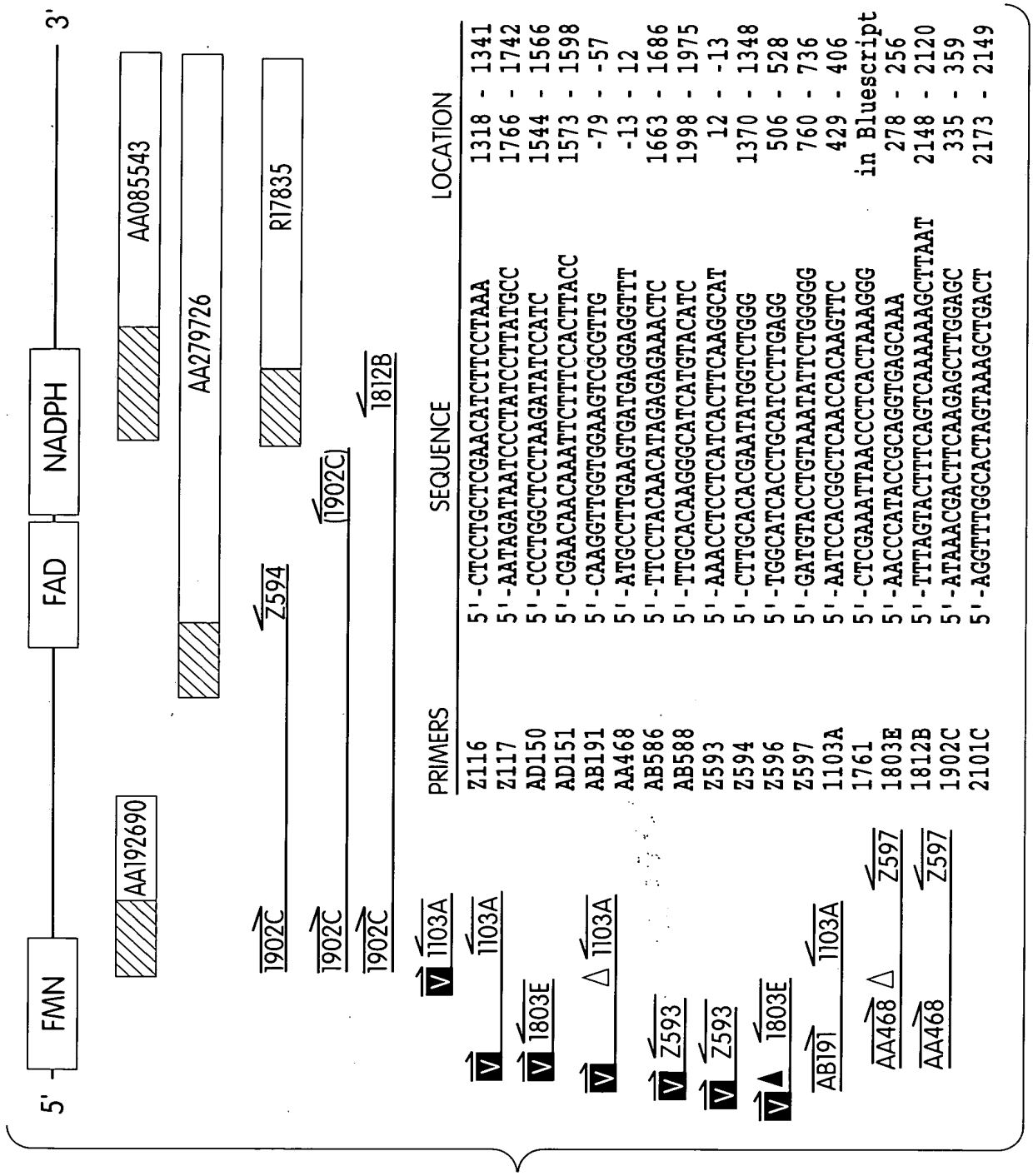


Fig. 1



PRIMERS	SEQUENCE	LOCATION
Z116	5'-CTCCTGCTCGAACATCTTCCTAAA	1318 - 1341
Z117	5'-AATAGATAATCCCTATCCTTATGCC	1766 - 1742
AD150	5'-CCCTGGCTCCTAAGATATCCATC	1544 - 1566
AD151	5'-CGAACAACAAATTCTTTCCACTTACC	1573 - 1598
AB191	5'-CAAGGTTGGTGGAAGTCGCGTTG	-79 - -57
AA468	5'-ATGCCTTGAAGTGATGAGGAGGTTT	-13 - 12
AB586	5'-TTCCTACAACATAGAGAGAAACTC	1663 - 1686
AB588	5'-TTGCACAAGGGCATCATGTACATC	1998 - 1975
Z593	5'-AAACCTCCTCATCACTTCAAGGCAT	12 - -13
Z594	5'-CTTGCACACGAATATGGTCTGGG	1370 - 1348
Z596	5'-TGGCATCACCTGCATCCTTGAGG	506 - 528
Z597	5'-GATGTACCTGTAAATATTCTGGGGG	760 - 736
1103A	5'-AATCCACGGCTCAACCACAAGTTC	429 - 406
1761	5'-CTCGAAATTAACCCTCACTAAAGGG	in Bluescript
1803E	5'-AACCCATACCGCAGGTGAGCAAA	278 - 256
1812B	5'-TTTAGTACTTTCAGTCAAAAAAGCTTAAT	2148 - 2120
1902C	5'-ATAAACGACTTCAAGAGCTTGGAGC	335 - 359
2101C	5'-AGGTTTGGCACTAGTAAAGCTGACT	2173 - 2149

Fig. 2

```
                                                                  CAAGGTTGGTGGAAGTCGCGTTGTGCAGGTTCGTGCCCGGCTGGCGCGGCGTGGTTTCACTGTTACATGCCTTGAAGTG
   1 ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGGACAGGCAAAGGCCATCGCAGAAGAAATGTGTGAGCAAGCTGTGGTACATGGATTTTCTGCAGATCTTCACTGTATTAGTGAA
     M  R  R  F  L  L  L  Y  A  T  Q  Q  G  Q  A  K  A  I  A  E  E  M  C  E  Q  A  V  V  H  G  F  S  A  D  L  H  C  I  S  E  40
 121 TCCGATAAGTATGACCTAAAAACCGAAACAGCTCCTCTTGTTGTTGTGGTTTCTACCACGGGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTTAAGGAAATACAGAACCAAACA
     S  D  K  Y  D  L  K  T  E  T  A  P  L  V  V  V  V  S  T  T  G  T  G  D  P  P  D  T  A  R  K  F  V  K  E  I  Q  N  Q  T  80
 241 CTGCCGGTTGATTTCTTTGCTCACCTGCGGTATGGGTTACTGGGTCTCGGTGATTCAGAATACACCTACTTTTGCAATGGGGGGAAGATAATTGATAAACGACTTCAAGAGCTTGGAGCC
     L  P  V  D  F  F  A  H  L  R  Y  G  L  L  G  L  G  D  S  E  Y  T  Y  F  C  N  G  G  K  I  I  D  K  R  L  Q  E  L  G  A  120
 361 CGGCATTTCTATGACACTGGACATGCAGATGACTGTGTAGGTTTAGAACTTGTGGTTGAGCCGTGGATTGCTGGACTCTGGCCAGCCCTCAGAAAGCATTTTAGGTCAAGCAGAGGACAA
     R  H  F  Y  D  T  G  H  A  D  D  C  V  G  L  E  L  V  V  E  P  W  I  A  G  L  W  P  A  L  R  K  H  F  R  S  S  R  G  Q  160
 481 GAGGAGATAAGTGGCGCACTCCCGGTGGCATCACCTGCATCCTTGAGGACAGACCTTGTGAAGTCAGAGCTGCTACACATTGAATCTCAAGTCGAGCTTCTGAGATTCGATGATTCAGGA
     E  E  I  S  G  A  L  P  V  A  S  P  A  S  L  R  T  D  L  V  K  S  E  L  L  H  I  E  S  Q  V  E  L  L  R  F  D  D  S  G  200
 601 AGAAAGGATTCTGAGGTTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAATGTTGTAATTGAAGACTTTGAGTCCTCACTTACCCGTTCGGTACCCCCACTCTCACAAGCCTCTCTG
     R  K  D  S  E  V  L  K  Q  N  A  V  N  S  N  Q  S  N  V  V  I  E  D  F  E  S  S  L  T  R  S  V  P  P  L  S  Q  A  S  L  240
 721 AATATTCCTGGTTTACCCCCAGAATATTTACAGGTACATCTGCAGGAGTCTCTTGGCCAGGAGGAAAGCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTTCAAGTGCCAATTTCAAAG
     N  I  P  G  L  P  P  E  Y  L  Q  V  H  L  Q  E  S  L  G  Q  E  E  S  Q  V  S  V  T  S  A  D  P  V  F  Q  V  P  I  S  K  280
 841 GCAGTTCAACTTACTACGAATGATGCCATAAAAACCACTCTGCTGGTAGAATTGGACATTTCAAATACAGACTTTTCCTATCAGCCTGGAGATGCCTTCAGCGTGATCTGCCCTAACAGT
     A  V  Q  L  T  T  N  D  A  I  K  T  T  L  L  V  E  L  D  I  S  N  T  D  F  S  Y  Q  P  G  D  A  F  S  V  I  C  P  N  S  320
 961 GATTCTGAGGTACAAAGCCTACTCCAAAGACTGCAGCTTGAAGATAAAAGAGAGCACTGCGTCCTTTTGAAAATAAAGGCAGACACAAAGAAGAAAGGAGCTACCTTACCCCAGCATATA
     D  S  E  V  Q  S  L  L  Q  R  L  Q  L  E  D  K  R  E  H  C  V  L  L  K  I  K  A  D  T  K  K  K  G  A  T  L  P  Q  H  I  360
1081 CCTGCGGGATGTTCTCTCCAGTTCATTTTTACCTGGTGTCTTGAAATCCGAGCAATTCCTAAAAAGGCATTTTTGCGAGCCCTTGTGGACTATACCAGTGACAGTGCTGAAAAGCGCAGG
     P  A  G  C  S  L  Q  F  I  F  T  W  C  L  E  I  R  A  I  P  K  K  A  F  L  R  A  L  V  D  Y  T  S  D  S  A  E  K  R  R  400
1201 CTACAGGAGCTGTGCAGTAAACAAGGGGCAGCCGATTATAGCCGCTTTGTACGAGATGCCTGTGCCTGCTTGTTGGATCTCCTCCTCGCTTTCCCTTCTTGCCAGCCACCACTCAGTCTC
     L  Q  E  L  C  S  K  Q  G  A  A  D  Y  S  R  F  V  R  D  A  C  A  C  L  L  D  L  L  L  A  F  P  S  C  Q  P  P  L  S  L  440
```

Fig. 3-1

```
1321 CTGCTCGAACATCTTCCTAAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTATTTCACCCAGGAAAGCTCCATTTTGTCTTCAACATTGTGGAATTTCTGTCTACTGCCACA
     L  L  E  H  L  P  K  L  Q  P  R  P  Y  S  C  A  S  S  S  L  F  H  P  G  K  L  H  F  V  F  N  I  V  E  F  L  S  T  A  T  480
1441 ACAGAGGTTCTGCGGAAGGGAGTATGTACAGGCTGGCTGGCCTTGTTGGTTGCTTCAGTTCTTCAGCCAAACATACATGCATCCCATGAAGACAGCGGGAAAGCCCTGGCTCCTAAGATA
     T  E  V  L  R  K  G  V  C  T  G  W  L  A  L  L  V  A  S  V  L  Q  P  N  I  H  A  S  H  E  D  S  G  K  A  L  A  P  K  I  520
1561 TCCATCTCTCCTCGAACAACAAATTCTTTCCACTTACCAGATGACCCCTCAATCCCCATCATAATGGTGGGTCCAGGAACCGGCATAGCCCCGTTTATTGGGTTCCTACAACATAGAGAG
     S  I  S  P  R  T  T  N  S  F  H  L  P  D  D  P  S  I  P  I  I  M  V  G  P  G  T  G  I  A  P  F  I  G  F  L  Q  H  R  E  560
1681 AAACTCCAAGAACAACACCCAGATGGAAATTTTGGAGCAATGTGGTTGTTTTTTGGCTGCAGGCATAAGGATAGGGATTATCTATTCAGAAAAGAGCTCAGACATTTCCTTAAGCATGGG
     K  L  Q  E  Q  H  P  D  G  N  F  G  A  M  W  L  F  F  G  C  R  H  K  D  R  D  Y  L  F  R  K  E  L  R  H  F  L  K  H  G  600
1801 ATCTTAACTCATCTAAAGGTTTCCTTCTCAAGAGATGCTCCTGTTGGGGAGGAGGAAGCCCCAGCAAAGTATGTACAAGACAACATCCAGCTTCATGGCCAGCAGGTGGCGAGAATCCTC
     I  L  T  H  L  K  V  S  F  S  R  D  A  P  V  G  E  E  E  A  P  A  K  Y  V  Q  D  N  I  Q  L  H  G  Q  Q  V  A  R  I  L  640
1921 CTCCAGGAGAACGGCCATATTTATGTGTGTGGAGATGCAAAGAATATGGCCAAGGATGTACATGATGCCCTTGTGCAAATAATAAGCAAAGAGGTTGGAGTTGAAAAACTAGAAGCAATG
     L  Q  E  N  G  H  I  Y  V  C  G  D  A  K  N  M  A  K  D  V  H  D  A  L  V  Q  I  I  S  K  E  V  G  V  E  K  L  E  A  M  680
2041 AAAACCCTGGCCACTTTAAAAGAAGAAAAACGCTACCTTCAGGATATTTGGTCATAAAACCAGAAATTAAAGAAAGAGGATTAAGCTTTTTTGACTGAAAGTACTAAAAGTCAGCTTTAC
     K  T  L  A  T  L  K  E  E  K  R  Y  L  Q  D  I  W  S  ***
2161 TAGTGCCAAACCTTTAAATTTTCAAAAGAAAATTTTCTTTCAACATTTCTTGAAGGACATGGAGTGGAGATTGGATCATTTAACAATATAACAAAACTTCCTGATTTGATTTTACGTATC
2281 TTCTATCTACGCCCTTCCTGTGCCTGTGACTCTCCCCAAATTGCCCTGTTGCCTTGAGCTCTTCTGAGCTAAAGGCAGCCTTCAGTCCCTATCAGCGCCTCCTTTACTTCCCAGAGAACT
2401 TCACAGAGACTCTGTCCTTCCATGCAAAGGCTTCCTGAAATAGGGGAGACTGACTGAGTAGCTCATTCTTGTGACTTACAGTGCCAACATTTAAAAAAGTATGAAAATGATTTATTTTTA
2521 TATGATGTATACCCATAAAGAATGCTCATATTAATGTACTTAAATTACACATGTAGAGCATATCTGTTATATGTTTATGTAACTATCAAATGGTTATTTGTTACTAAAGCTATATTTCTG
2641 ATAAAAAATATTTTAGGATAATTGCCTACAGAGGGATTTATTTTTATGATGCTGGGAAATATGAAATGTATTTTAAAATTTCACTCTGGGCATATGGATTTATCTATCACCATTACTTTT
2761 TTTTAAGTCACAATTTCAGAATTTTGGGACATTTGCATTCAATTTACAGGTACCAGTACGTACATATTTTAATAGAAAGATACAACCTTTTTATTTTCACTCCTTTTATTTCTGCTGCTT
2881 GGCACATTTTTGAGTTTTCCCACATTATTTGTCTCCATGATACCACTCAAGCAGTGTGCTGGACCTAAAATACTGACTTTAGTTAGTATCCTTGGATTTTTAGATTCCCCAGTGTCTAAT
3001 TCCCTGTTATAATTTGCACAAACAAAACAAAATGTTATGATAATCTTTCTCCACTGTTCTAATATATATTGTATTTTTATTTGATAGCTTGGGATTTAAAACATCTCTGTTGAAGGCTTT
3121 TGATCCTTTTGAGAAATAAAGATCTGAAAGAAATGGCATAATCTTAAAAAAAAAAAAAAA
```

Fig. 3-2

```
                                                                  CAAGGTTGGTGGAAGTCGCGTTGTGCAGGTTCGTGCCCGGCTGGCGCGGCGTGGTTTCACTGTTACATGCCTTGAAGTG
   1 ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGGACAGGCAAAGGCCATCGCAGAAGAAATGTGTGAGCAAGCTGTGGTACATGGATTTTCTGCAGATCTTCACTGTATTAGTGAA
     M  R  R  F  L  L  L  Y  A  T  Q  Q  G  Q  A  K  A  I  A  E  E  M  C  E  Q  A  V  V  H  G  F  S  A  D  L  H  C  I  S  E  40

 121 TCCGATAAGTATGACCTAAAAACCGAAACAGCTCCTCTTGTTGTTGTGGTTTCTACCACGGGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTTAAGGAAATACAGAACCAAACA
     S  D  K  Y  D  L  K  T  E  T  A  P  L  V  V  V  V  S  T  T  G  T  G  D  P  P  D  T  A  R  K  F  V  K  E  I  Q  N  Q  T  80

 241 CTGCCGGTTGATTTCTTTGCTCACCTGCGGTATGGGTTACTGGGTCTCGGTGATTCAGAATACACCTACTTTTGCAATGGGGGGAAGATAATTGATAAACGACTTCAAGAGCTTGGAGCC
     L  P  V  D  F  F  A  H  L  R  Y  G  L  L  G  L  G  D  S  E  Y  T  Y  F  C  N  G  G  K  I  I  D  K  R  L  Q  E  L  G  A  120

 361 CGGCATTTCTATGACACTGGACATGCAGATGACTGTGTAGGTTTAGAACTTGTGGTTGAGCCGTGGATTGCTGGACTCTGGCCAGCCCTCAGAAAGCATTTTAGGTCAAGCAGAGGACAA
     R  H  F  Y  D  T  G  H  A  D  D  C  V  G  L  E  L  V  V  E  P  W  I  A  G  L  W  P  A  L  R  K  H  F  R  S  S  R  G  Q  160

 481 GAGGAGATAAGTGGCGCACTCCCGGTGGCATCACCTGCATCCTTGAGGACAGACCTTGTGAAGTCAGAGCTGCTACACATTGAATCTCAAGTCGAGCTTCTGAGATTCGATGATTCAGGA
     E  E  I  S  G  A  L  P  V  A  S  P  A  S  L  R  T  D  L  V  K  S  E  L  L  H  I  E  S  Q  V  E  L  L  R  F  D  D  S  G  200

 601 AGAAAGGATTCTGAGGTTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAATGTTGTAATTGAAGACTTTGAGTCCTCACTTACCCGTTCGGTACCCCCACTCTCACAAGCCTCTCTG
     R  K  D  S  E  V  L  K  Q  N  A  V  N  S  N  Q  S  N  V  V  I  E  D  F  E  S  S  L  T  R  S  V  P  P  L  S  Q  A  S  L  240

 721 AATATTCCTGGTTTACCCCCAGAATATTTACAGGTACATCTGCAGGAGTCTCTTGGCCAGGAGGAAAGCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTTCAAGTGCCAATTTCAAAG
     N  I  P  G  L  P  P  E  Y  L  Q  V  H  L  Q  E  S  L  G  Q  E  E  S  Q  V  S  V  T  S  A  D  P  V  F  Q  V  P  I  S  K  280

 841 GCAGTTCAACTTACTACGAATGATGCCATAAAAACCACTCTGCTGGTAGAATTGGACATTTCAAATACAGACTTTTCCTATCAGCCTGGAGATGCCTTCAGCGTGATCTGCCCTAACAGT
     A  V  Q  L  T  T  N  D  A  I  K  T  T  L  L  V  E  L  D  I  S  N  T  D  F  S  Y  Q  P  G  D  A  F  S  V  I  C  P  N  S  320

 961 GATTCTGAGGTACAAAGCCTACTCCAAAGACTGCAGCTTGAAGATAAAAGAGAGCACTGCGTCCTTTTGAAAATAAAGGCAGACACAAAGAAGAAAGGAGCTACCTTACCCCAGCATATA
     D  S  E  V  Q  S  L  L  Q  R  L  Q  L  E  D  K  R  E  H  C  V  L  L  K  I  K  A  D  T  K  K  K  G  A  T  L  P  Q  H  I  360

1081 CCTGCGGGATGTTCTCTCCAGTTCATTTTTACCTGGTGTCTTGAAATCCGAGCAATTCCTAAAAAGGCATTTTTGCGAGCCCTTGTGGACTATACCAGTGACAGTGCTGAAAAGCGCAGG
     P  A  G  C  S  L  Q  F  I  F  T  W  C  L  E  I  R  A  I  P  K  K  A  F  L  R  A  L  V  D  Y  T  S  D  S  A  E  K  R  R  400

1201 CTACAGGAGCTGTGCAGTAAACAAGGGGCAGCCGATTATAGCCGCTTTGTACGAGATGCCTGTGCCTGCTTGTTGGATCTCCTCCTCGCTTTCCCTTCTTGCCAGCCACCACTCAGTCTC
     L  Q  E  L  C  S  K  Q  G  A  A  D  Y  S  R  F  V  R  D  A  C  A  C  L  L  D  L  L  L  A  F  P  S  C  Q  P  P  L  S  L  440
```

Fig. 3-3

```
1321 CTGCTCGAACATCTTCCTAAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTATTTCACCCAGGAAAGCTCCATTTTGTCTTCAACATTGTGGAATTTCTGTCTACTGCCACA
     L  L  E  H  L  P  K  L  Q  P  R  P  Y  S  C  A  S  S  S  L  F  H  P  G  K  L  H  F  V  F  N  I  V  E  F  L  S  T  A  T  480

1441 ACAGAGGTTCTGCGGAAGGGAGTATGTACAGGCTGGCTGGCCTTGTTGGTTGCTTCAGTTCTTCAGCCAAACATACATGCATCCCATGAAGACAGCGGGAAAGCCCTGGCTCCTAAGATA
     T  E  V  L  R  K  G  V  C  T  G  W  L  A  L  L  V  A  S  V  L  Q  P  N  I  H  A  S  H  E  D  S  G  K  A  L  A  P  K  I  520

1561 TCCATCTCTCCTCGAACAACAAATTCTTTCCACTTACCAGATGACCCCTCAATCCCCATCATAATGGTGGGTCCAGGAACCGGCATAGCCCCGTTTATTGGGTTCCTACAACATAGAGAG
     S  I  S  P  R  T  T  N  S  F  H  L  P  D  D  P  S  I  P  I  I  M  V  G  P  G  T  G  I  A  P  F  I  G  F  L  Q  H  R  E  560

1681 AAACTCCAAGAACAACACCCAGATGGAAATTTTGGAGCAATGTGGTTGTTTTTTGGCTGCAGGCATAAGGATAGGGATTATCTATTCAGAAAAGAGCTCAGACATTTCCTTAAGCATGGG
     K  L  Q  E  Q  H  P  D  G  N  F  G  A  M  W  L  F  F  G  C  R  H  K  D  R  D  Y  L  F  R  K  E  L  R  H  F  L  K  H  G  600

1801 ATCTTAACTCATCTAAAGGTTTCCTTCTCAAGAGATGCTCCTGTTGGGGAGGAGGAAGCCCCAGCAAAGTATGTACAAGACAACATCCAGCTTCATGGCCAGCAGGTGGCGAGAATCCTC
     I  L  T  H  L  K  V  S  F  S  R  D  A  P  V  G  E  E  E  A  P  A  K  Y  V  Q  D  N  I  Q  L  H  G  Q  Q  V  A  R  I  L  640

1921 CTCCAGGAGAACGGCCATATTTATGTGTGTGGAGATGCAAAGAATATGGCCAAGGATGTACATGATGCCCTTGTGCAAATAATAAGCAAAGAGGTTGGAGTTGAAAAACTAGAAGCAATG
     L  Q  E  N  G  H  I  Y  V  C  G  D  A  K  N  M  A  K  D  V  H  D  A  L  V  Q  I  I  S  K  E  V  G  V  E  K  L  E  A  M  680

2041 AAAACCCTGGCCACTTTAAAAGAAGAAAAACGCTACCTTCAGGATATTTGGTCATAAAACCAGAAATTAAAGAAAGAGGATTAAGCTTTTTTGACTGAAAGTACTAAAAGTCAGCTTTAC
     K  T  L  A  T  L  K  E  E  K  R  Y  L  Q  D  I  W  S  ***

2161 TAGTGCCAAACCTTTAAATTTTCAAAAGAAAATTTTCTTTCAACATTTCTTGAAGGACATGGAGTGGAGATTGGATCATTTAACAATATAACAAAACTTCCTGATTTGATTTTACGTATC
2281 TTCTATCTACGCCCTTCCTGTGCCTGTGACTCTCCCCAAATTGCCCTGTTGCCTTGAGCTCTTCTGAGCTAAAGGCAGCCTTCAGTCCCTATCAGCGCCTCCTTTACTTCCCAGAGAACT
2401 TCACAGAGACTCTGTCCTTCCATGCAAAGGCTTCCTGAAATAGGGGAGACTGACTGAGTAGCTCATTCTTGTGACTTACAGTGCCAACATTTAAAAAAGTATGAAAATGATTTATTTTTA
2521 TATGATGTATACCCATAAAGAATGCTCATATTAATGTACTTAAATTACACATGTAGAGCATATCTGTTATATGTTTATGTAACTATCAAATGGTTATTTGTTACTAAAGCTATATTTCTG
2641 ATAAAAAATATTTTAGGATAATTGCCTACAGAGGGATTTATTTTTATGATGCTGGGAAATATGAAATGTATTTTAAAATTTCACTCTGGGCATATGGATTTATCTATCACCATTACTTTT
2761 TTTTAAGTCACAATTTCAGAATTTTGGGACATTTGCATTCAATTTACAGGTACCAGTACGTACATATTTTAATAGAAAGATACAACCTTTTTATTTTCACTCCTTTTATTTCTGCTGCTT
2881 GGCACATTTTTGAGTTTTCCCACATTATTTGTCTCCATGATACCACTCAAGCAGTGTGCTGGACCTAAAATACTGACTTTAGTTAGTATCCTTGGATTTTTAGATTCCCCAGTGTCTAAT
3001 TCCCTGTTATAATTTGCACAAACAAAACAAAATGTTATGATAATCTTTCTCCACTGTTCTAATATATATTGTATTTTTATTTGATAGCTTGGGATTTAAAACATCTCTGTTGAAGGCTTT
3121 TGATCCTTTTGAGAAATAAAGATCTGAAAGAAATGGCATAATCTTAAAAAAAAAAAAAAA
```

Fig. 3-4

```
HsMTRR      ------------------------------------------------
CeMTRR      ------------------------------------------------
HsCPR       MGDSHVDTSSTVSEAVAEEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEE   50
                                                  FMN
HsMTRR      -------------------------MRRFLLLYATQQGQAKAIAEEMCE   24
CeMTRR      -------------------------MTDFLIAFGSQTGQAETIAKSLKE   24
HsCPR       VPEFTKIQTLTSSVRESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSK  100
                                       .. ...* * *   *. .
                                                FMN
HsMTRR      QAVVHGFSADLHCISESDK-YDLKT-------ETAPLVVVVSTTGTGDPP   66
CeMTRR      KAELIGLTPRLHALDENEKKFNLNE-------EKLC-AIVVSSTGDGDAP   66
HsCPR       DAHRYG----MRGMSADPEEYDLADLSSLPEIDNALVVFCMATYGEGDPT  146
             *   *    .  . .  . ..* .      .        ... * **
                                        FMN
HsMTRR      DTARKFVKEIQNQTLPVDFFAHLRYGLLGLGDSEYTYFCNGGKIIDKRLQ  116
CeMTRR      DNCARFVRRINRNSLENEYLKNLDYVLLGLGDSNYSSYQTIPRKIDKQLT  116
HsCPR       DNAQDFYDWLQETDVD---LSGVKFAVFGLGNKTYEHFNAMGKYVDKRLE  193
            *   *   ..   .       . . . ***.  *  .    . .** *

HsMTRR      ELGARHFYDTGHADDCVGLELVVEPWIAGLWPALRKHFRSSRGQEEISGA  166
CeMTRR      ALGANRLFDRAEADDQVGLELEVEPWIEKFFATLASRFDISADKMN----  162
HsCPR       QLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEHF----------GV  233
             ***   .. . .**   **     *    .  .   *

HsMTRR      LPVASPASLRTDLVKSELLHIESQVELL--RFDDSGRKDSEVLKQNAVNS  214
CeMTRR      -AITESSNLKLNQVKTE----EEKKALLQKRIEDEESDDEGRGRVIGID-  206
HsCPR       EATGEESSIRQYEL------------VVHTDIDAAKVYMGEMGRLKSYEN  271
                  . ..   .             ..    .          .  . .

HsMTRR      NQSNVVIEDF---ESSLTRSVPPLS-QASLNIPGLPPEYLQVHLQESLGQ  260
CeMTRR      ---MLIPEHYDYPEISLLKGSQTLSNDENLRVPIAPQPFIVSSVSNRKLP  253
HsCPR       QKP-----PFD----------------------AKNPFLAAVTTNRKLN  293
                    .                          ..     .

HsMTRR      EESQVS-------VTSADPVFQVPISKAVQLTT--NDAIKTTLLVELDIS  301
CeMTRR      EDTKLEWQNLCKMPGVVTKPFEVLVVSAEFVTDPFSKKIKTKRMITVDFG  303
HsCPR       QGTE-----------------------------------RHLMHLELD  306
            . .                                       .. ..

HsMTRR      N--TDFSYQPGDAFSVICPNSDSEVQSLLQR-LQLEDKREHCVLLKIKAD  348
CeMTRR      DHAAELQYEPGDAIYFCVPNPALEVNFILKRCGVLDIADQQCEL-SINPK  352
HsCPR       ISDSKIRYESGDHVAVYPANDSALVNQLGK---ILGADLD--VVMSLNNL  351
               .   *. **       *    *. .     *    .   .  .

HsMTRR      TKKKGATLPQHIPAGCSLQFIFTWCLEIRAIPKKAFLRALVDYTSDSAEK  398
CeMTRR      TEKINAQIPGHVHKITTLRHMFTTCLDIRRAPGRPLIRVLAESTSDPNEK  402
HsCPR       DEESNKKHP--FPCPTSYRTALTYYLDITNPPRTNVLYELAQYASEPSEQ  399
                    *      . .   *  *.*   *    .  * . .*.  *
```

Fig. 4-1

```
HsMTRR      RRLQEL--CSKQGAADYSRFVRDACACLLDLLLAFPSCQPPLSLLLEHLP  446
CeMTRR      RRLLEL--CSAQGMKDFTDFVRTPGLSLADMLFAFPNVKPPVDRLIELLP  450
HsCPR       ELLRKMASSSGEGKELYLSWVVEARRHILAILQDCPSLRPPIDHLCELLP  449
              *  .   * .*   .  .*      .  .*   *   **.  * * **
                       FAD          FAD          FAD
HsMTRR      KLQPRPYSCASSSLFHPGKLHFVFNIVEFLSTATTEVLRKGVCTGWLALL  496
CeMTRR      RLIPRPYSMSS---YENRKARLIYSEMEFPATDGRRHSRKGLATDWLNSL  497
HsCPR       RLQARYYSIASSSKVHPNSVHICAVVVEYETKAGR--INKGVATNWL---  494
            .*  * **  *                .*. .       **. * **

HsMTRR      VASVLQPNIHASHEDSGKALAPKISISPRTTNSFHLP-------DDPSIP  539
CeMTRR      R------------------IGDKVQVLGKEPARFRLPPLGMTKNSAGKLP  529
HsCPR       RAKE------PVGENGGRALVPMFVRKSQFRLPFK-----------ATTP  527
                             .                *               *
                    NADPH
HsMTRR      IIMVGPGTGIAPFIGFLQHREKLQEQHPDGNFGAMW-LFFGCRHKDRDYL  588
CeMTRR      LLMVGPGTGVSVFLSFLHFLRKLKQDSPSDFVDVPRVLFFGCRDSSVDAI  579
HsCPR       VIMVGPGTGVAPFIGFIQERAWLRQQGKE---VGETLLYYGCRRSDEDYL  574
            ..*******.. *. *.     * ..           *..***    * .
                              NADPH          NADPH
HsMTRR      FRKELRHFLKHGILTHLKVSFSRDAPVGEEEAPAKYVQDNIQLHGQQVAR  638
CeMTRR      YMSELEMFVSEGILTDLIICESEQ--------KGERVQDGLRKYLDKVLP  621
HsCPR       YREELAQFHRDGALTQLNVAFSRE------QSHKVYVQHLLKQDREHLWK  618
            .  **  *   * ** * .  * *           **  .    . .
                      NADPH
HsMTRR      ILLQE-NGHIYVCGDAKNMAKDVHDALVQIISKEVGVEKLEAMKTLATLK  687
CeMTRR      FLTASTESKIFICGDAKGMSKDVWQCFSDIVASDQGIPDLEAKKKLMDLK  671
HsCPR       LI--EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQAVDYIKKLM  666
             .     . *..****. *..** .   .*..   ..   .*   .  *
              NADPH/FAD
HsMTRR      EEKRYLQDIWS   698
CeMTRR      KSDQYIEDVWG   682
HsCPR       TKGRYSLDVWS   677
               *  *.*
```

Fig. 4-2

```
HsMTRR  ----------------------------------------------------
CeMTRR  ----------------------------------------------------
HsCPR   MGDSHVDTSSTVSEAVAEEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEE   50
                                                  FMN
HsMTRR  -------------------------MRRFLLLYATQQGQAKAIAEEMCE   24
CeMTRR  -------------------------MTDFLIAFGSQTGQAETIAKSLKE   24
HsCPR   VPEFTKIQTLTSSVRESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSK  100
                                     .. ...* * *   *. .
                                                FMN
HsMTRR  QAVVHGFSADLHCISESDK-YDLKT-------ETAPLVVVVSTTGTGDPP   66
CeMTRR  KAELIGLTPRLHALDENEKKFNLNE-------EKLC-AIVVSSTGDGDAP   66
HsCPR   DAHRYG----MRGMSADPEEYDLADLSSLPEIDNALVVFCMATYGEGDPT  146
         *   *     .  . .  . ..* .       .        ... * **
                                        FMN
HsMTRR  DTARKFVKEIQNQTLPVDFFAHLRYGLLGLGDSEYTYFCNGGKIIDKRLQ  116
CeMTRR  DNCARFVRRINRNSLENEYLKNLDYVLLGLGDSNYSSYQTIPRKIDKQLT  116
HsCPR   DNAQDFYDWLQETDVD---LSGVKFAVFGLGNKTYEHFNAMGKYVDKRLE  193
        *    *   ..   .       . . . ***.  *  .    . .** *

HsMTRR  ELGARHFYDTGHADDCVGLELVVEPWIAGLWPALRKHFRSSRGQEEISGA  166
CeMTRR  ALGANRLFDRAEADDQVGLELEVEPWIEKFFATLASRFDISADKMN----  162
HsCPR   QLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEHF----------GV  233
         ***    .. . .**   **     *    .  .   *

HsMTRR  LPVASPASLRTDLVKSELLHIESQVELL--RFDDSGRKDSEVLKQNAVNS  214
CeMTRR  -AITESSNLKLNQVKTE----EEKKALLQKRIEDEESDDEGRGRVIGID-  206
HsCPR   EATGEESSIRQYEL-----------VVHTDIDAAKVYMGEMGRLKSYEN  271
              . ..   .            ..    .          .  . .

HsMTRR  NQSNVVIEDF---ESSLTRSVPPLS-QASLNIPGLPPEYLQVHLQESLGQ  260
CeMTRR  ---MLIPEHYDYPEISLLKGSQTLSNDENLRVPIAPQPFIVSSVSNRKLP  253
HsCPR   QKP-----PFD----------------------AKNPFLAAVTTNRKLN  293
                 .                                 ..    .

HsMTRR  EESQVS-------VTSADPVFQVPISKAVQLTT--NDAIKTTLLVELDIS  301
CeMTRR  EDTKLEWQNLCKMPGVVTKPFEVLVVSAEFVTDPFSKKIKTKRMITVDFG  303
HsCPR   QGTE-----------------------------------RHLMHLELD  306
        . .                                          .. ..

HsMTRR  N--TDFSYQPGDAFSVICPNSDSEVQSLLQR-LQLEDKREHCVLLKIKAD  348
CeMTRR  DHAAELQYEPGDAIYFCVPNPALEVNFILKRCGVLDIADQQCEL-SINPK  352
HsCPR   ISDSKIRYESGDHVAVYPANDSALVNQLGK---ILGADLD--VVMSLNNL  351
           .   *. **       *    *. .     *    .   .  .

HsMTRR  TKKKGATLPQHIPAGCSLQFIFTWCLEIRAIPKKAFLRALVDYTSDSAEK  398
CeMTRR  TEKINAQIPGHVHKITTLRHMFTTCLDIRRAPGRPLIRVLAESTSDPNEK  402
HsCPR   DEESNKKHP--FPCPTSYRTALTYYLDITNPPRTNVLYELAQYASEPSEQ  399
               *      . .   *  *.*   *    .  * . .*.  *
```

Fig. 4-3

```
HsMTRR      RRLQEL--CSKQGAADYSRFVRDACACLLDLLLAFPSCQPPLSLLLEHLP  446
CeMTRR      RRLLEL--CSAQGMKDFTDFVRTPGLSLADMLFAFPNVKPPVDRLIELLP  450
HsCPR       ELLRKMASSSGEGKELYLSWVVEARRHILAILQDCPSLRPPIDHLCELLP  449
              *  .   * .*   .  .*      .  .*   *   **.  * * **
                      FAD              FAD             FAD
HsMTRR      KLQPRPYSCASSSLFHPGKLHFVFNIVEFLSTATTEVLRKGVCTGWLALL  496
CeMTRR      RLIPRPYSMSS---YENRKARLIYSEMEFPATDGRRHSRKGLATDWLNSL  497
HsCPR       RLQARYYSIASSSKVHPNSVHICAVVVEYETKAGR--INKGVATNWL---  494
            .*  * **  *                .*. .        **. * **

HsMTRR      VASVLQPNIHASHEDSGKALAPKISISPRTTNSFHLP-------DDPSIP  539
CeMTRR      R------------------IGDKVQVLGKEPARFRLPPLGMTKNSAGKLP  529
HsCPR       RAKE------PVGENGGRALVPMFVRKSQFRLPFK-----------ATTP  527
                             .              *              *
                    NADPH
HsMTRR      IIMVGPGTGIAPFIGFLQHREKLQEQHPDGNFGAMW-LFFGCRHKDRDYL  588
CeMTRR      LLMVGPGTGVSVFLSFLHFLRKLKQDSPSDFVDVPRVLFFGCRDSSVDAI  579
HsCPR       VIMVGPGTGVAPFIGFIQERAWLRQQGKE---VGETLLYYGCRRSDEDYL  574
            ..*******.. *. *.     * ..           *..***    * .
                                NADPH          NADPH
HsMTRR      FRKELRHFLKHGILTHLKVSFSRDAPVGEEEAPAKYVQDNIQLHGQQVAR  638
CeMTRR      YMSELEMFVSEGILTDLIICESEQ--------KGERVQDGLRKYLDKVLP  621
HsCPR       YREELAQFHRDGALTQLNVAFSRE------QSHKVYVQHLLKQDREHLWK  618
            .  **  *   * ** * .  * *           **  .    . .
                      NADPH
HsMTRR      ILLQE-NGHIYVCGDAKNMAKDVHDALVQIISKEVGVEKLEAMKTLATLK  687
CeMTRR      FLTASTESKIFICGDAKGMSKDVWQCFSDIVASDQGIPDLEAKKKLMDLK  671
HsCPR       LI--EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQAVDYIKKLM  666
             .     . *..****. *..** .   .*..   ..   .*   .  *
              NADPH/FAD
HsMTRR      EEKRYLQDIWS   698
CeMTRR      KSDQYIEDVWG   682
HsCPR       TKGRYSLDVWS   677
               *  *.*
```

Fig. 4-4

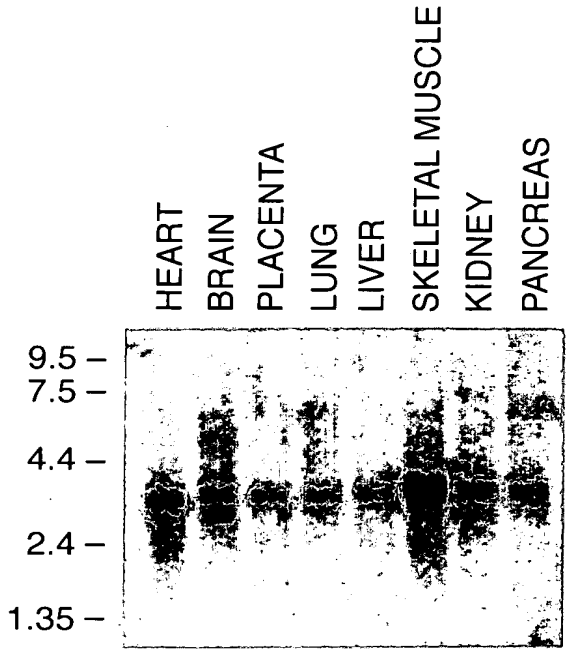


Fig. 5A

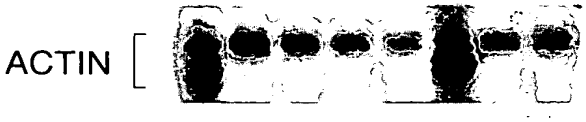


Fig. 5B

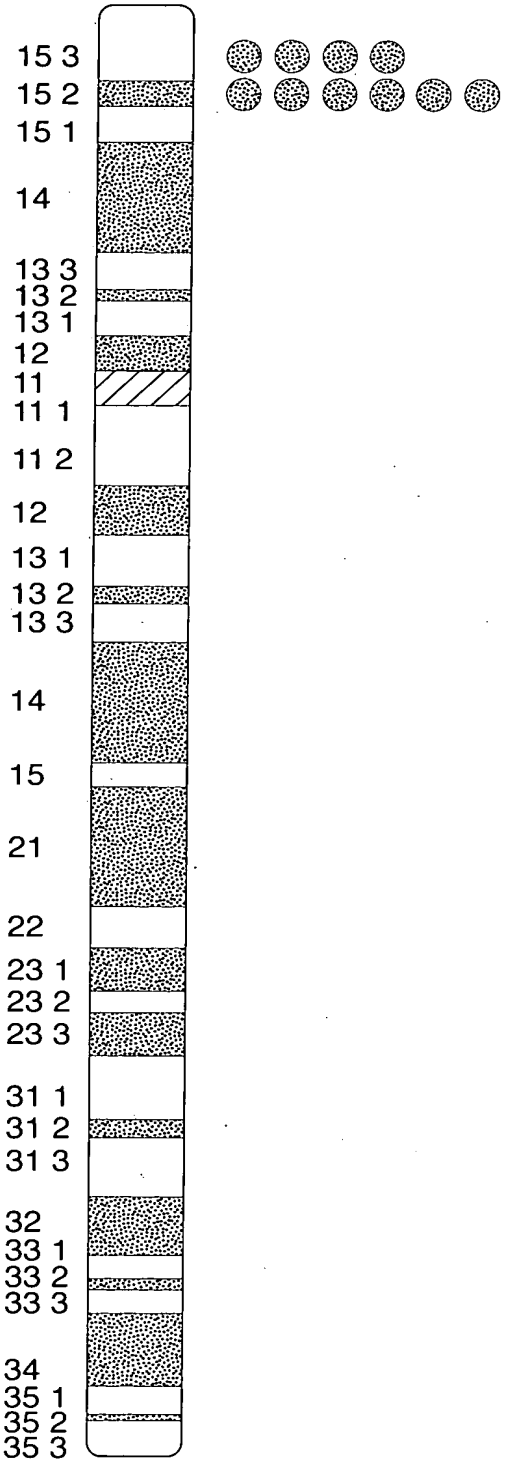


Fig. 6

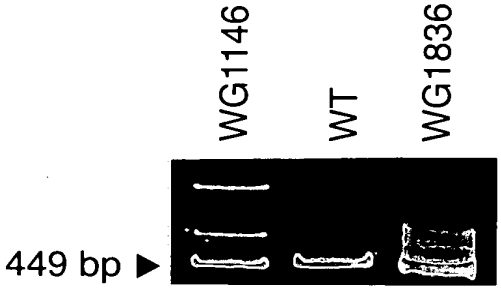


Fig. 7A

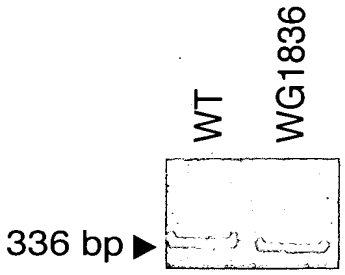


Fig. 7B

Position	Sequence	Accession#	Protein	Organism
572	GAMW**L**FFGCRHKDRDYLF	(AF025794)	MTRR	(H sapiens)
558	GETL**L**YYGCRRSDEDYLY	(A60557)	CPR	(H sapiens)
559	GETL**L**YYGCRRAAEDYLY	(D00101)	CPR	(O cuniculus)
560	GESI**L**YFGCRKRSEDYIY	(X93090)	CPR	(D melanogaster)
572	GPAL**L**FFGCRNRQMDFIY	(P37116)	CPR	(V radiata)
573	GPTV**L**FFGCRKSDEDFLY	(Z26938)	CPR	(A niger)
1281	CPMV**L**VFGCRQSKIDHIY	(D16408)	NOS I	(H sapiens)
1009	GRMT**L**VFGCRRPDEDHIY	(U05810)	NOS II	(H sapiens)
1040	TPMT**L**VFGCRCSQLDHLY	(L26914)	NOS III	(H sapiens)
380	GRMT**L**VFGCRHPEEDHLY	(U85094)	NOS	(O cuniculus)
1005	GDMI**L**LFGCRHPDMDHIY	(U46504)	NOS	(G gallus)
481	GKNW**L**FFGNPHFTEDFLY	(M23008)	SR	(E coli)
915	GEVF**L**YLGSRHKREEYLY	(L26503)	SR	(S cerevisiae)
407	GRNW**L**IFGNRHFHRDFLY	(Z23169)	SR	(T roseopersicina)
261	GLAW**L**FLGVANVDSLLYD	(X99419)	FNR	(P sativum)
251	GLAW**L**FLGVPTSSSLLYK	(P00455)	FNR	(S oleracea)

Fig. 7C

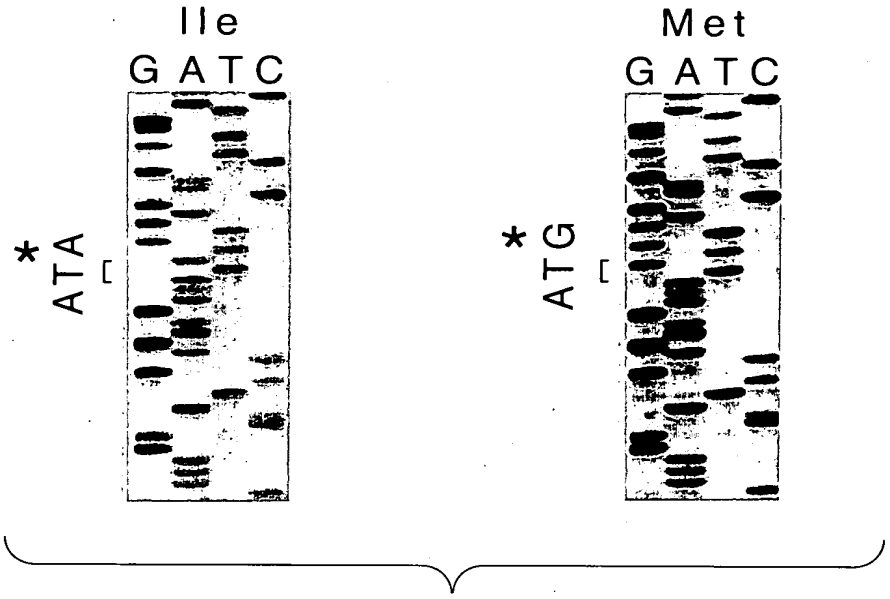


Fig. 8A

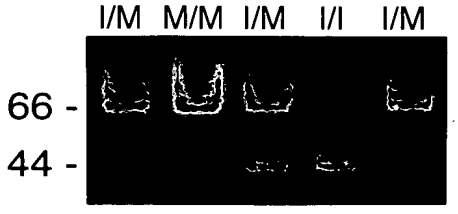


Fig. 8B